

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/573,135
Source: IFWP
Date Processed by STIC: 4/26/06

ENTERED



IFWP

RAW SEQUENCE LISTING

DATE: 04/26/2006

PATENT APPLICATION: US/10/573,135

TIME: 07:31:36

Input Set : F:\39670a.txt

Output Set : N:\CRF4\04262006\J573135.raw

5 <110> APPLICANT: Alitalo et al
 7 <120> TITLE OF INVENTION: VEGF-C OR VEGF-D MATERIALS AND METHODS FOR OLIGODENDROCYTES
 9 <130> FILE REFERENCE: 28967/39670A
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/573,135
 C--> 11 <141> CURRENT FILING DATE: 2006-03-23
 11 <160> NUMBER OF SEQ ID NOS: 38
 13 <170> SOFTWARE: PatentIn version 3.0
 15 <210> SEQ ID NO: 1
 16 <211> LENGTH: 2772
 17 <212> TYPE: DNA
 18 <213> ORGANISM: Homo sapiens
 20 <220> FEATURE:
 21 <221> NAME/KEY: CDS
 22 <222> LOCATION: (1)..(2772)
 24 <400> SEQUENCE: 1
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 26 Met Glu Arg Gly Leu Pro Leu Leu Cys Ala Val Leu Ala Leu Val Leu
 27 1 5 10 15
 29 gcc ccg gcc ggc gct ttt cgc aac gat gaa tgt ggc gat act ata aaa 96
 30 Ala Pro Ala Gly Ala Phe Arg Asn Asp Glu Cys Gly Asp Thr Ile Lys
 31 20 25 30
 33 att gaa agc ccc ggg tac ctt aca tct cct ggt tat cct cat tct tat 144
 34 Ile Glu Ser Pro Gly Tyr Leu Thr Ser Pro Gly Tyr Pro His Ser Tyr
 35 35 40 45
 37 cac cca agt gaa aaa tgc gaa tgg ctg att cag gct ccg gac cca tac 192
 38 His Pro Ser Glu Lys Cys Glu Trp Leu Ile Gln Ala Pro Asp Pro Tyr
 39 50 55 60
 41 cag aga att atg atc aac ttc aac cct cac ttc gat ttg gag gac aga 240
 42 Gln Arg Ile Met Ile Asn Phe Asn Pro His Phe Asp Leu Glu Asp Arg
 43 65 70 75 80
 45 gac tgc aag tat gac tac gtg gaa gtc ttc gat gga gaa aat gaa aat 288
 46 Asp Cys Lys Tyr Asp Tyr Val Glu Val Phe Asp Gly Glu Asn Glu Asn
 47 85 90 95
 49 gga cat ttt agg gga aag ttc tgt gga aag ata gcc cct cct cct gtt 336
 50 Gly His Phe Arg Gly Lys Phe Cys Gly Lys Ile Ala Pro Pro Pro Val
 51 100 105 110
 53 gtg tct tca ggg cca ttt ctt ttt atc aaa ttt gtc tct gac tac gaa 384
 54 Val Ser Ser Gly Pro Phe Leu Phe Ile Lys Phe Val Ser Asp Tyr Glu
 55 115 120 125
 57 aca cat ggt gca gga ttt tcc ata cgt tat gaa att ttc aag aga ggt 432
 58 Thr His Gly Ala Gly Phe Ser Ile Arg Tyr Glu Ile Phe Lys Arg Gly
 59 130 135 140
 61 cct gaa tgt tcc cag aac tac aca aca cct agt gga gtg ata aag tcc 480

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62	Pro	Glu	Cys	Ser	Gln	Asn	Tyr	Thr	Thr	Pro	Ser	Gly	Val	Ile	Lys	Ser	
63	145					150					155					160	
65	ccc	gga	ttc	cct	gaa	aaa	tat	ccc	aac	agc	ctt	gaa	tgc	act	tat	att	528
66	Pro	Gly	Phe	Pro	Glu	Lys	Tyr	Pro	Asn	Ser	Leu	Glu	Cys	Thr	Tyr	Ile	
67					165					170					175		
69	gtc	ttt	gcg	cca	aag	atg	tca	gag	att	atc	ctg	gaa	ttt	gaa	agc	ttt	576
70	Val	Phe	Ala	Pro	Lys	Met	Ser	Glu	Ile	Ile	Leu	Glu	Phe	Glu	Ser	Phe	
71					180					185					190		
73	gac	ctg	gag	cct	gac	tca	aat	cct	cca	ggg	ggg	atg	ttc	tgt	cgc	tac	624
74	Asp	Leu	Glu	Pro	Asp	Ser	Asn	Pro	Pro	Gly	Gly	Met	Phe	Cys	Arg	Tyr	
75					195					200					205		
77	gac	cgg	cta	gaa	atc	tgg	gat	gga	ttc	cct	gat	gtt	ggc	cct	cac	att	672
78	Asp	Arg	Leu	Glu	Ile	Trp	Asp	Gly	Phe	Pro	Asp	Val	Gly	Pro	His	Ile	
79		210					215					220					
81	ggg	cgt	tac	tgt	gga	cag	aaa	aca	cca	ggg	cga	atc	cga	tcc	tca	tcg	720
82	Gly	Arg	Tyr	Cys	Gly	Gln	Lys	Thr	Pro	Gly	Arg	Ile	Arg	Ser	Ser	Ser	
83	225					230					235					240	
85	ggc	att	ctc	tcc	atg	gtt	ttt	tac	acc	gac	agc	gcg	ata	gca	aaa	gaa	768
86	Gly	Ile	Leu	Ser	Met	Val	Phe	Tyr	Thr	Asp	Ser	Ala	Ile	Ala	Lys	Glu	
87					245						250				255		
89	ggg	ttc	tca	gca	aac	tac	agt	gtc	ttg	cag	agc	agt	gtc	tca	gaa	gat	816
90	Gly	Phe	Ser	Ala	Asn	Tyr	Ser	Val	Leu	Gln	Ser	Ser	Val	Ser	Glu	Asp	
91					260					265					270		
93	ttc	aaa	tgt	atg	gaa	gct	ctg	ggc	atg	gaa	tca	gga	gaa	att	cat	tct	864
94	Phe	Lys	Cys	Met	Glu	Ala	Leu	Gly	Met	Glu	Ser	Gly	Glu	Ile	His	Ser	
95					275					280					285		
97	gac	cag	atc	aca	gct	tct	tcc	cag	tat	agc	acc	aac	tgg	tct	gca	gag	912
98	Asp	Gln	Ile	Thr	Ala	Ser	Ser	Gln	Tyr	Ser	Thr	Asn	Trp	Ser	Ala	Glu	
99		290					295					300					
101	cgc	tcc	cgc	ctg	aac	tac	cct	gag	aat	ggg	tgg	act	ccc	gga	gag	gat	960
102	Arg	Ser	Arg	Leu	Asn	Tyr	Pro	Glu	Asn	Gly	Trp	Thr	Pro	Gly	Glu	Asp	
103	305					310					315					320	
105	tcc	tac	cga	gag	tgg	ata	cag	gta	gac	ttg	ggc	ctt	ctg	cgc	ttt	gtc	1008
106	Ser	Tyr	Arg	Glu	Trp	Ile	Gln	Val	Asp	Leu	Gly	Leu	Leu	Arg	Phe	Val	
107					325						330				335		
109	acg	gct	gtc	ggg	aca	cag	ggc	gcc	att	tca	aaa	gaa	acc	aag	aag	aaa	1056
110	Thr	Ala	Val	Gly	Thr	Gln	Gly	Ala	Ile	Ser	Lys	Glu	Thr	Lys	Lys	Lys	
111					340					345				350			
113	tat	tat	gtc	aag	act	tac	aag	atc	gac	gtt	agc	tcc	aac	ggg	gaa	gac	1104
114	Tyr	Tyr	Val	Lys	Thr	Tyr	Lys	Ile	Asp	Val	Ser	Ser	Asn	Gly	Glu	Asp	
115					355					360				365			
117	tgg	atc	acc	ata	aaa	gaa	gga	aac	aaa	cct	gtt	ctc	ttt	cag	gga	aac	1152
118	Trp	Ile	Thr	Ile	Lys	Glu	Gly	Asn	Lys	Pro	Val	Leu	Phe	Gln	Gly	Asn	
119					370					375				380			
121	acc	aac	ccc	aca	gat	gtt	gtg	gtt	gca	gta	ttc	ccc	aaa	cca	ctg	ata	1200
122	Thr	Asn	Pro	Thr	Asp	Val	Val	Val	Ala	Val	Phe	Pro	Lys	Pro	Leu	Ile	
123	385					390					395				400		
125	act	cga	ttt	gtc	cga	atc	aag	cct	gca	act	tgg	gaa	act	ggc	ata	tct	1248
126	Thr	Arg	Phe	Val	Arg	Ile	Lys	Pro	Ala	Thr	Trp	Glu	Thr	Gly	Ile	Ser	

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127		405		410		415		
129	atg aga ttt gaa gta tac ggt tgc aag ata aca gat tat cct tgc tct							1296
130	Met Arg Phe Glu Val Tyr Gly Cys Lys Ile Thr Asp Tyr Pro Cys Ser							
131		420		425		430		
133	gga atg ttg ggt atg gtg tct gga ctt att tct gac tcc cag atc aca							1344
134	Gly Met Leu Gly Met Val Ser Gly Leu Ile Ser Asp Ser Gln Ile Thr							
135		435		440		445		
137	tca tcc aac caa gga gac aga aac tgg atg cct gaa aac atc cgc ctg							1392
138	Ser Ser Asn Gln Gly Asp Arg Asn Trp Met Pro Glu Asn Ile Arg Leu							
139		450		455		460		
141	gta acc agt cgc tct ggc tgg gca ctt cca ccc gca cct cat tcc tac							1440
142	Val Thr Ser Arg Ser Gly Trp Ala Leu Pro Pro Ala Pro His Ser Tyr							
143	465		470		475		480	
145	atc aat gag tgg ctg caa ata gac ctg ggg gag gag aag atc gtg agg							1488
146	Ile Asn Glu Trp Leu Gln Ile Asp Leu Gly Glu Glu Lys Ile Val Arg							
147		485		490		495		
149	ggc atc atc att cag ggt ggg aag cac cga gag aac aag gtg ttc atg							1536
150	Gly Ile Ile Ile Gln Gly Gly Lys His Arg Glu Asn Lys Val Phe Met							
151		500		505		510		
153	agg aag ttc aag atc ggg tac agc aac aac ggc tcg gac tgg aag atg							1584
154	Arg Lys Phe Lys Ile Gly Tyr Ser Asn Asn Gly Ser Asp Trp Lys Met							
155		515		520		525		
157	atc atg gat gac agc aaa cgc aag gcg aag tct ttt gag ggc aac aac							1632
158	Ile Met Asp Asp Ser Lys Arg Lys Ala Lys Ser Phe Glu Gly Asn Asn							
159		530		535		540		
161	aac tat gat aca cct gag ctg cgg act ttt cca gct ctg tcc acg cga							1680
162	Asn Tyr Asp Thr Pro Glu Leu Arg Thr Phe Pro Ala Leu Ser Thr Arg							
163	545		550		555		560	
165	ttc atc agg atc tac ccc gag aga gcc act cat ggc gga ctg ggg ctg							1728
166	Phe Ile Arg Ile Tyr Pro Glu Arg Ala Thr His Gly Gly Leu Gly Leu							
167		565		570		575		
169	aga atg gag ctg ctg ggc tgt gaa gtg gaa gcc cct aca gct gga ccg							1776
170	Arg Met Glu Leu Leu Gly Cys Glu Val Glu Ala Pro Thr Ala Gly Pro							
171		580		585		590		
173	acc act ccc aac ggg aac ttg gtg gat gaa tgt gat gac gac cag gcc							1824
174	Thr Thr Pro Asn Gly Asn Leu Val Asp Glu Cys Asp Asp Asp Gln Ala							
175		595		600		605		
177	aac tgc cac agt gga aca ggt gat gac ttc cag ctg aca ggt ggc acc							1872
178	Asn Cys His Ser Gly Thr Gly Asp Asp Phe Gln Leu Thr Gly Gly Thr							
179		610		615		620		
181	act gtg ctg gcc aca gaa aag ccc acg gtc ata gac agc acc ata caa							1920
182	Thr Val Leu Ala Thr Glu Lys Pro Thr Val Ile Asp Ser Thr Ile Gln							
183	625		630		635		640	
185	tca gag ttt cca aca tat ggt ttt aac tgt gaa ttt ggc tgg ggc tct							1968
186	Ser Glu Phe Pro Thr Tyr Gly Phe Asn Cys Glu Phe Gly Trp Gly Ser							
187		645		650		655		
189	cac aag acc ttc tgc cac tgg gaa cat gac aat cac gtg cag ctg aag							2016
190	His Lys Thr Phe Cys His Trp Glu His Asp Asn His Val Gln Leu Lys							
191		660		665		670		

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194 Trp Ser Val Leu Thr Ser Lys Thr Gly Pro Ile Gln Asp His Thr Gly
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197 gat ggc aac ttc atc tat tcc caa gct gac gaa aat cag aag ggc aaa      2112
198 Asp Gly Asn Phe Ile Tyr Ser Gln Ala Asp Glu Asn Gln Lys Gly Lys
199      690      695      700
201 gtg gct cgc ctg gtg agc cct gtg gtt tat tcc cag aac tct gcc cac      2160
202 Val Ala Arg Leu Val Ser Pro Val Val Tyr Ser Gln Asn Ser Ala His
203 705      710      715      720
205 tgc atg acc ttc tgg tat cac atg tct ggg tcc cac gtc ggc aca ctc      2208
206 Cys Met Thr Phe Trp Tyr His Met Ser Gly Ser His Val Gly Thr Leu
207      725      730      735
209 agg gtc aaa ctg cgc tac cag aag cca gag gag tac gat cag ctg gtc      2256
210 Arg Val Lys Leu Arg Tyr Gln Lys Pro Glu Glu Tyr Asp Gln Leu Val
211      740      745      750
213 tgg atg gcc att gga cac caa ggt gac cac tgg aag gaa ggg cgt gtc      2304
214 Trp Met Ala Ile Gly His Gln Gly Asp His Trp Lys Glu Gly Arg Val
215      755      760      765
217 ttg ctc cac aag tct ctg aaa ctt tat cag gtg att ttc gag ggc gaa      2352
218 Leu Leu His Lys Ser Leu Lys Leu Tyr Gln Val Ile Phe Glu Gly Glu
219      770      775      780
221 atc gga aaa gga aac ctt ggt ggg att gct gtg gat gac att agt att      2400
222 Ile Gly Lys Gly Asn Leu Gly Gly Ile Ala Val Asp Asp Ile Ser Ile
223 785      790      795      800
225 aat aac cac att tca caa gaa gat tgt gca aaa cca gca gac ctg gat      2448
226 Asn Asn His Ile Ser Gln Glu Asp Cys Ala Lys Pro Ala Asp Leu Asp
227      805      810      815
229 aaa aag aac cca gaa att aaa att gat gaa aca ggg agc acg cca gga      2496
230 Lys Lys Asn Pro Glu Ile Lys Ile Asp Glu Thr Gly Ser Thr Pro Gly
231      820      825      830
233 tac gaa ggt gaa gga gaa ggt gac aag aac atc tcc agg aag cca ggc      2544
234 Tyr Glu Gly Glu Gly Glu Gly Asp Lys Asn Ile Ser Arg Lys Pro Gly
235      835      840      845
237 aat gtg ttg aag acc tta gaa ccc atc ctc atc acc atc ata gcc atg      2592
238 Asn Val Leu Lys Thr Leu Glu Pro Ile Leu Ile Thr Ile Ile Ala Met
239      850      855      860
241 agc gcc ctg ggg gtc ctc ctg ggg gct gtc tgt ggg gtc gtg ctg tac      2640
242 Ser Ala Leu Gly Val Leu Leu Gly Ala Val Cys Gly Val Val Leu Tyr
243 865      870      875      880
245 tgt gcc tgt tgg cat aat ggg atg tca gaa aga aac ttg tct gcc ctg      2688
246 Cys Ala Cys Trp His Asn Gly Met Ser Glu Arg Asn Leu Ser Ala Leu
247      885      890      895
249 gag aac tat aac ttt gaa ctt gtg gat ggt gtg aag ttg aaa aaa gac      2736
250 Glu Asn Tyr Asn Phe Glu Leu Val Asp Gly Val Lys Leu Lys Lys Asp
251      900      905      910
253 aaa ctg aat aca cag agt act tat tcg gag gca tga      2772
254 Lys Leu Asn Thr Gln Ser Thr Tyr Ser Glu Ala
255      915      920
258 <210> SEQ ID NO: 2

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259 <211> LENGTH: 923

260 <212> TYPE: PRT

261 <213> ORGANISM: Homo sapiens

263 <400> SEQUENCE: 2

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270          20          25          30
273 Ile Glu Ser Pro Gly Tyr Leu Thr Ser Pro Gly Tyr Pro His Ser Tyr
274          35          40          45
277 His Pro Ser Glu Lys Cys Glu Trp Leu Ile Gln Ala Pro Asp Pro Tyr
278          50          55          60
281 Gln Arg Ile Met Ile Asn Phe Asn Pro His Phe Asp Leu Glu Asp Arg
282 65          70          75          80
285 Asp Cys Lys Tyr Asp Tyr Val Glu Val Phe Asp Gly Glu Asn Glu Asn
286          85          90          95
289 Gly His Phe Arg Gly Lys Phe Cys Gly Lys Ile Ala Pro Pro Pro Val
290          100         105         110
293 Val Ser Ser Gly Pro Phe Leu Phe Ile Lys Phe Val Ser Asp Tyr Glu
294          115         120         125
297 Thr His Gly Ala Gly Phe Ser Ile Arg Tyr Glu Ile Phe Lys Arg Gly
298          130         135         140
301 Pro Glu Cys Ser Gln Asn Tyr Thr Thr Pro Ser Gly Val Ile Lys Ser
302 145          150         155         160
305 Pro Gly Phe Pro Glu Lys Tyr Pro Asn Ser Leu Glu Cys Thr Tyr Ile
306          165         170         175
310 Val Phe Ala Pro Lys Met Ser Glu Ile Ile Leu Glu Phe Glu Ser Phe
311          180         185         190
314 Asp Leu Glu Pro Asp Ser Asn Pro Pro Gly Gly Met Phe Cys Arg Tyr
315          195         200         205
319 Asp Arg Leu Glu Ile Trp Asp Gly Phe Pro Asp Val Gly Pro His Ile
320          210         215         220
323 Gly Arg Tyr Cys Gly Gln Lys Thr Pro Gly Arg Ile Arg Ser Ser Ser
324 225         230         235         240
327 Gly Ile Leu Ser Met Val Phe Tyr Thr Asp Ser Ala Ile Ala Lys Glu
328          245         250         255
331 Gly Phe Ser Ala Asn Tyr Ser Val Leu Gln Ser Ser Val Ser Glu Asp
332          260         265         270
335 Phe Lys Cys Met Glu Ala Leu Gly Met Glu Ser Gly Glu Ile His Ser
336          275         280         285
339 Asp Gln Ile Thr Ala Ser Ser Gln Tyr Ser Thr Asn Trp Ser Ala Glu
340          290         295         300
343 Arg Ser Arg Leu Asn Tyr Pro Glu Asn Gly Trp Thr Pro Gly Glu Asp
344 305          310         315         320
347 Ser Tyr Arg Glu Trp Ile Gln Val Asp Leu Gly Leu Leu Arg Phe Val
348          325         330         335
351 Thr Ala Val Gly Thr Gln Gly Ala Ile Ser Lys Glu Thr Lys Lys Lys
352          340         345         350
355 Tyr Tyr Val Lys Thr Tyr Lys Ile Asp Val Ser Ser Asn Gly Glu Asp

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VERIFICATION SUMMARY

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L:11 M:270 C: Current Application Number differs, Replaced Current Application No

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date